

Figure 1

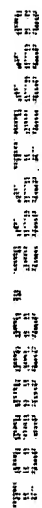
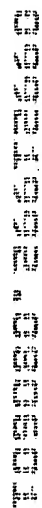
[illegible][illegible]

Figure 4

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Ecgcpe :MHNQAPICRRKSTRIYVGNVPIGDG : 25
 Atgcpe : MATGVLPAPVSGIKIPDSKVGFKSMNLVRICDVRSLRSARRVSVIRNSQGSDLAELQPASEGSPLLVPRQKYCESLHKTVRRTVVMVGNVALGSE : 100

Ecgcpe : APTAVQSMNVRITTDVEATVNOQKAMERVGADIVRVSVPTMDAAEFKLKKQOVNPLVADIHFDPALKVAEYGVDCIRINPKNIGN : 114
 Atgcpe : HPRIQVMTSDTKDITGTVDEVMRMDKADGADIVRTVOGKKKADACFEIKDKLVQLNINPLVADIHFAPVALRVAEC.FDKIRYNPKNFADRRQAQFE : 199

Ecgcpe :ERIRMVVCARDKNIPIRIGVNAGSLEKDPQEKYCEPFOALLSASMRHVDHLDEINFDQFKVSVKASDVFTAVESYRLIAKQ : 198
 Atgcpe : TIDYTEDEYQKELQHIQVFTPLVEKQKKYGRAMRIGTNHGSISDRIMSYGDSPRGMVESAFEFARICRKLDAHNFEVFSMKASNPVIMVQAYRLLVAE : 298

Ecgcpe : I....DQPLHLGI TEAGGARS GAVKSAIGCGLLISECGDTERVSLAADPVEEIK : 249
 Atgcpe : MYVHGMDYPLHLGVTEAGEGEDGRMKSAIGCGLLIQDGGDTIRVSLTEPPEEIDPCRRLANLGTKAAKLOQCAPFEEKHRHYDFQRRTGDLFPVQKEG : 398

Ecgcpe : : -
 Atgcpe : EEVDYRNVLHRDGSVLMSSISLDQLKAPELLYRSLATKLVVGNPFKDLATVDSILLRELPPVDDQVARLALKRLIDVSMGVIAPLSEQLTPLPNAMVLVN : 498

Ecgcpe : : -
 Atgcpe : LKELSGGAYKLLPECTRLVVSRLRGDEPYEELEILKNIDATMILHDVPFTEDKVS RVHAARRLFEFLSENSVNFVPIHHINFPTGIHRDELVIHAGTYAGG : 598.

Ecgcpe :VGFDLKSILIRSRGINETACPTCSRQEFDVIGTVNAIEQRLLEDITTPMDVSGICGVNNGPGBALVSTLGVTCGNK : 325
 Atgcpe : LLVDGLGDGVMLEAPDQDFDLRNTSFNLQCGMRNRTKTEVXVSCPSCGRTLEDLQEISAEIREKTSHPG.VSNAIMGCI VNGPGBMADADFGYVGGSP : 697

Ecgcpe : .KSGIYEDG.VRKDRDNNNMIDCLEARIETAKASQLDEARRRDVQQVKK : 372
 Atgcpe : GKIDLVGKTVVRGGLAMTEATDALIGLIKEHG.....RWVDPPVADE : 740

Figure 4

RESULTS

pZL1 (135H1):

...[SalI/aaaaatcg(...)]gaaaaATGGCGACTGGAGTATTGCCAGTCCGGTTTCTGGGATCAAG
M A T G V L P A P V S G I K
ATACCGGATTTCGAAAGTCGGGTTTGGTAAAAGCATGAATCTTGTGAGAATTGTGATGTTAGGAGTCTA
I P D S K V G F G K S M N L V R I C D V R S L
BglII▼
AGATCTGCT(...)]GATGAGTAGatttc(...)]ataaaaagt(NotI)(XbaI)(BamHI)(HindIII)[**SphI**]...
R S A (...) D E *

pQE30:

...[SalI/aaaaatcg(...)]gaaaaATGGCGACTGGAGTATTGCCAGTCCGGTTTCTGGGATCAAG
M A T G V L P A P V S G I K
ATACCGGATTTCGAAAGTCGGGTTTGGTAAAAGCATGAATCTTGTGAGAATTGTGATGTTAGGAGTCTA
I P D S K V G F G K S M N L V R I C D V R S L
BamHI▼
AGATCTGCT(...)]GATGAGTAGatttc(...)]ataaaaagt(NotI)(XbaI)(BamHI)(HindIII)[**SphI**]...
R S A (...) D E *

pQE-AGH:

...[SalI/aaaaatcg(...)]gaaaaATGGCGACTGGAGTATTGCCAGTCCGGTTTCTGGGATCAAG
M A T G V L P A P V S G I K
ATACCGGATTTCGAAAGTCGGGTTTGGTAAAAGCATGAATCTTGTGAGAATTGTGATGTTAGGAGTCTA
I P D S K V G F G K S M N L V R I C D V R S L
BamHI/BglII▼
AGATCTGCT(...)]GATGAGTAGatttc(...)]ataaaaagt(NotI)(XbaI)(BamHI)(HindIII)[**SphI**]...
R S A (...) D E *

Figure 5